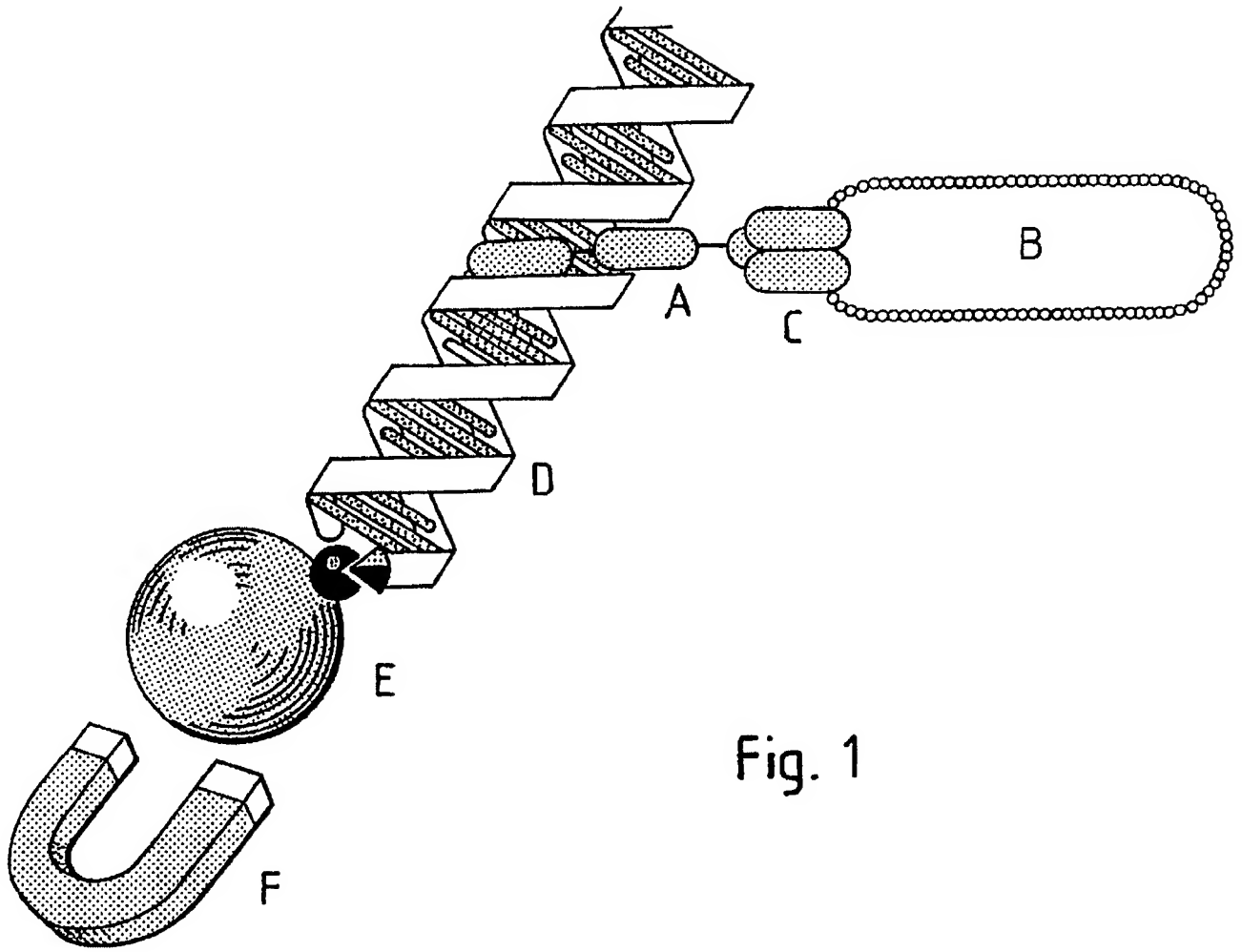


Fig. 1

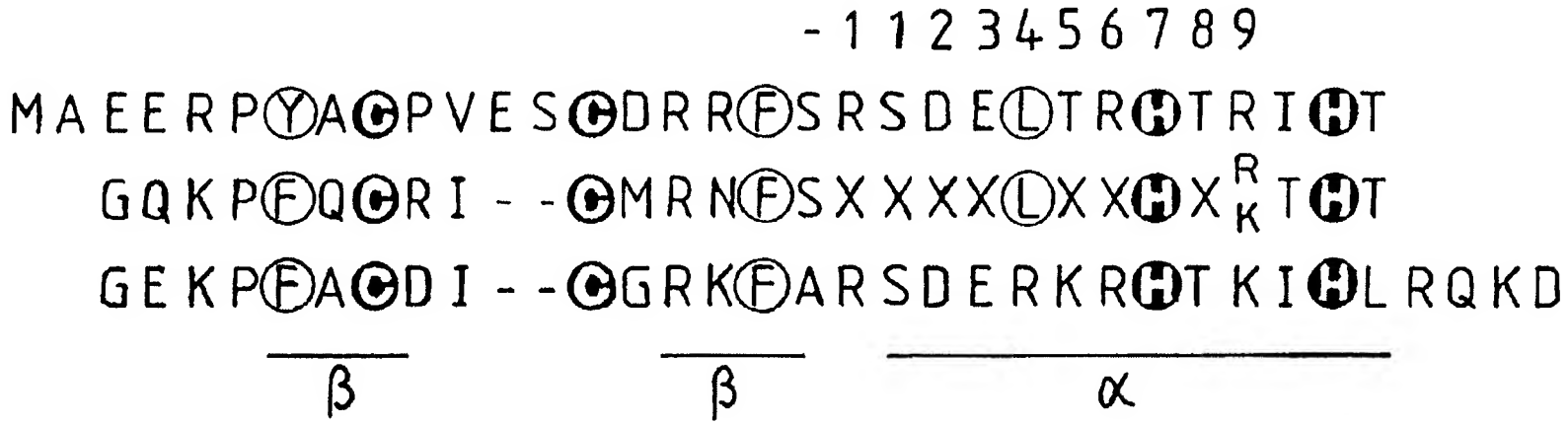

-1 1 2 3 4 5 6 7 8 9
MAEERPYACPVESCDRRFSRSDELTRHTRIHT
GQKPFQCRI--CMRNFSXXXXLXXHXR/KTHT
GEKPFACDI--CGRKFARSDERKRHTKIHLRQKD
β
β
α

Fig. 2

(i) TATGACTTGGATGGGAGACCGCCTGG
ACTGAACCTACCCTCTGGCGGACCTTAA –B

(ii) TATATAGCGTGGGCGTATATA
ATATATCGCACCCGCATATATGCG –B

(iii) TATATAGCGXXXGCGTATATA
ATATATCGCXXXCGCATATATGCG –B

Fig. 3

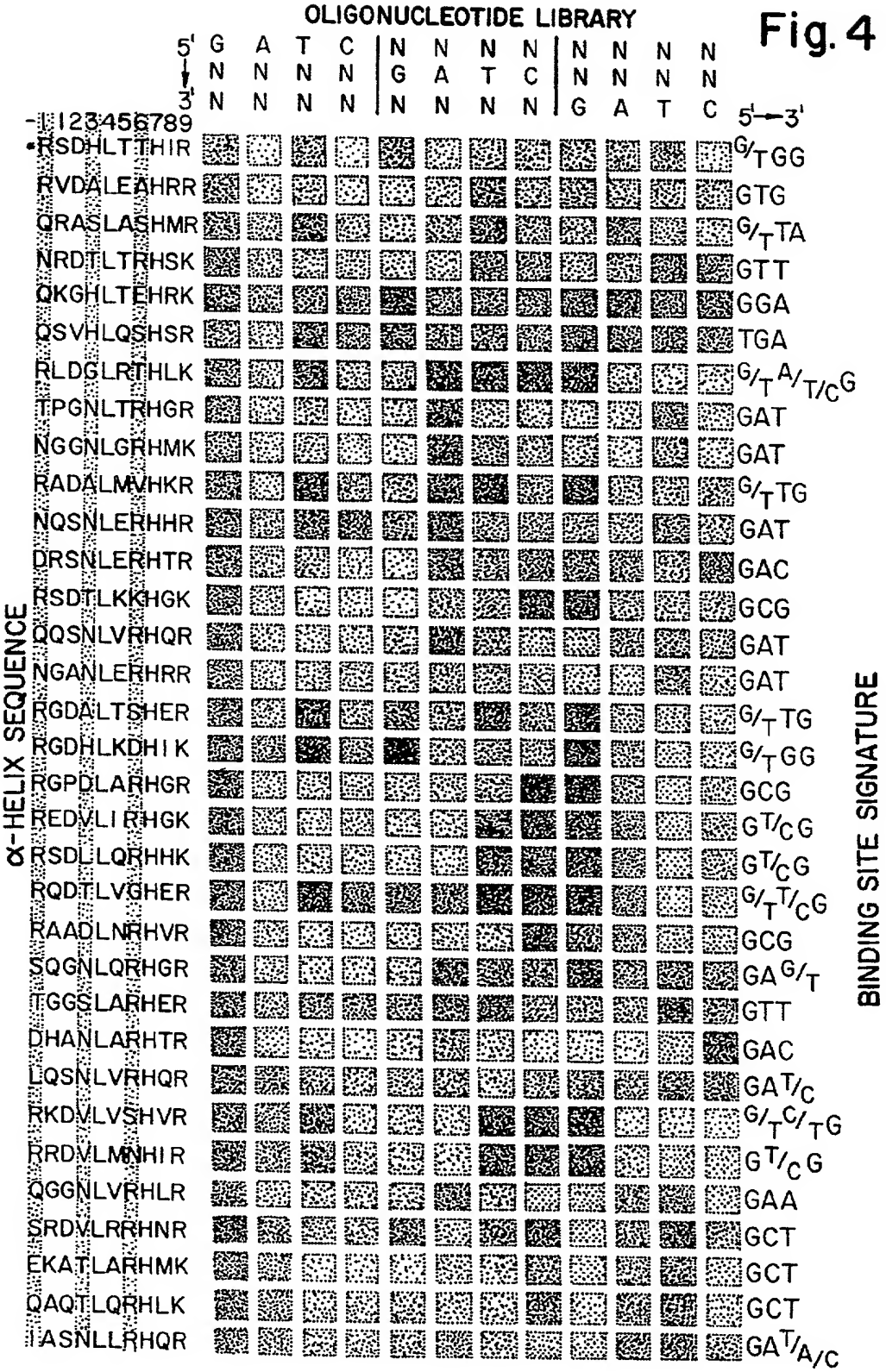

OLIGONUCLEOTIDE LIBRARY
5' G A T C | N N N N | N N N N
N N N N | G A T C | N N N N
3' N N N N | N N N N | G A T C
-1 1 2 3 4 5 6 7 8 9
α-HELIX SEQUENCE
BINDING SITE SIGNATURE
5'→3'
•RSDHLTTHIR G/TGG
RVDALEAHRR GTG
QRASLASHMR G/TTA
NRDTLTRHSK GTT
QKGHLTEHRK GGA
QSVHLQSHSR TGA
RLDGLRTHLK G/TA/T/CG
TPGNLTRHGR GAT
NGGNLGRHMK GAT
RADALMVHKR G/TTG
NQSNLERHHR GAT
DRSNLERHTR GAC
RSDTLKKHGK GCG
QQSNLVRHQR GAT
NGANLERHRR GAT
RGDALTSHER G/TTG
RGDHLKDHIK G/TGG
RGPDLARHGR GCG
REDVLIRHGK GT/CG
RSDLLQRHHK GT/CG
RQDTLVGHER G/TT/CG
RAADLNRHVR GCG
SQGNLQRHGR GAG/T
TGGSLARHER GTT
DHANLARHTR GAC
LQSNLVRHQR GAT/C
RKDVLVSHVR G/TC/TG
RRDVLMNHIR GT/CG
QGGNLVRHLR GAA
SRDVLRRHNR GCT
EKATLARHMK GCT
QAQTLQRHLK GCT
IASNLLRHQR GAT/A/C

Fig. 4

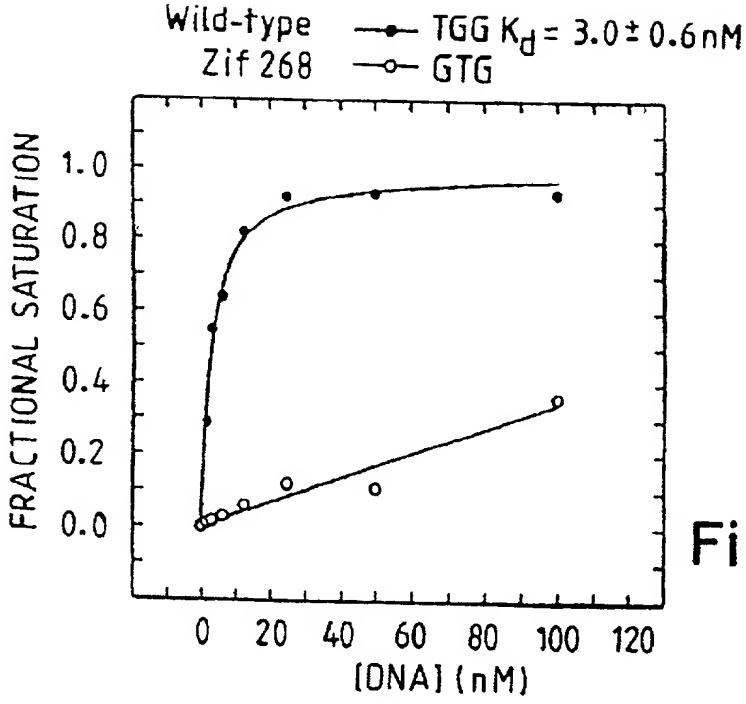

Wild-type
Zif 268
TGG K_d = 3.0 ± 0.6nM
GTG
FRACTIONAL SATURATION
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
120
[DNA] (nM)

Fig. 5A

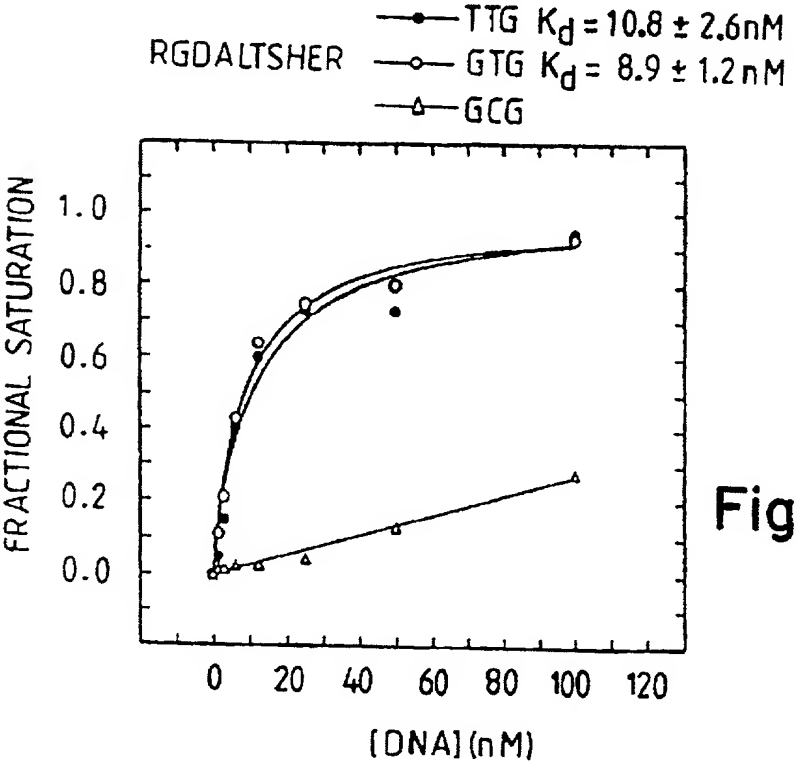

RGDALTSHER
TTG K_d = 10.8 ± 2.6nM
GTG K_d = 8.9 ± 1.2nM
GCG
FRACTIONAL SATURATION
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
120
[DNA] (nM)

Fig. 5B

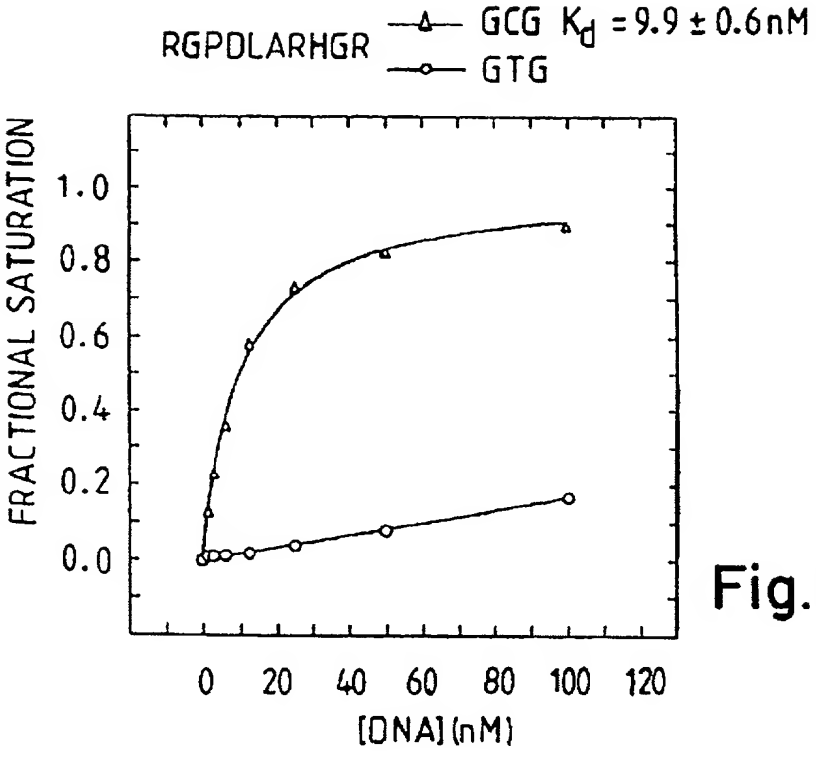

RGPDLARHGR
GCG K_d = 9.9 ± 0.6nM
GTG
FRACTIONAL SATURATION
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
120
[DNA] (nM)

Fig. 5C

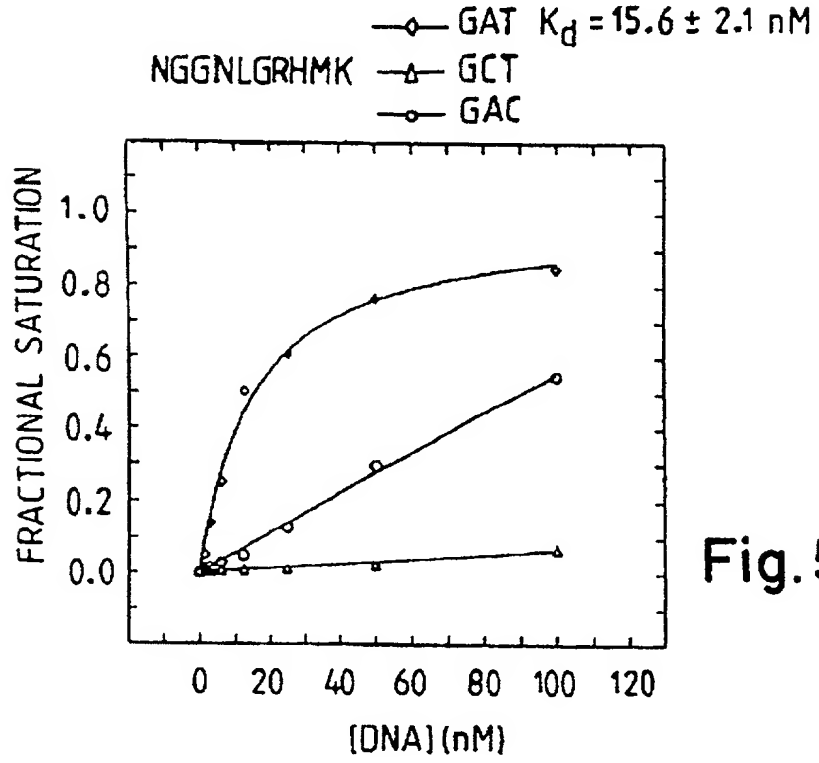

NGGNLGRHMK
GAT K_d = 15.6 ± 2.1 nM
GCT
GAC
FRACTIONAL SATURATION
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
120
[DNA] (nM)

Fig. 5D

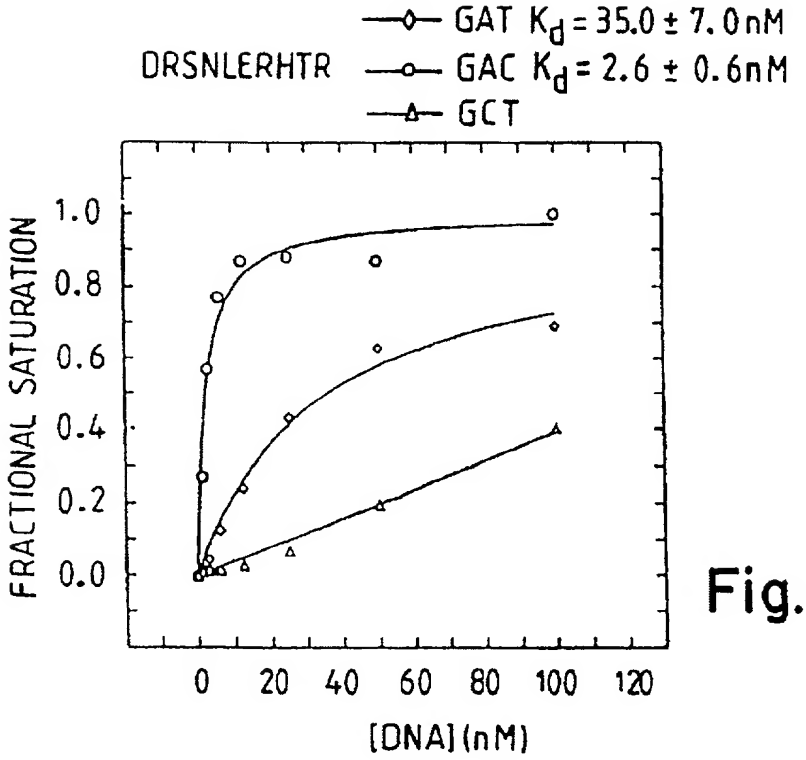

GAT K_d = 35.0 ± 7.0 nM
DRSNLERHTR
GAC K_d = 2.6 ± 0.6 nM
GCT
FRACTIONAL SATURATION
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
120
[DNA] (nM)

Fig. 5E

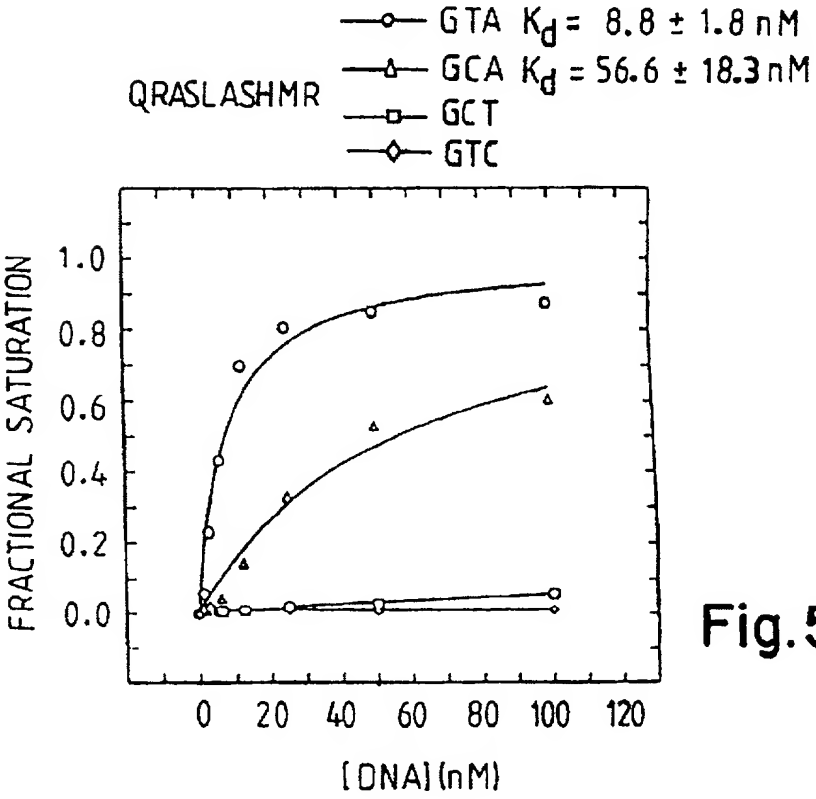

GTA K_d = 8.8 ± 1.8 nM
QRASLASHMR
GCA K_d = 56.6 ± 18.3 nM
GCT
GTC
FRACTIONAL SATURATION
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
120
[DNA] (nM)

Fig. 5F

1	*BCR - ABL*	TTC CAT GGA GAC GCA G AA GCC CTT CAG CGG CCA
2	*BCR*	TTC CAT GGA GAC GCA G gt gag ttc ctc acg cca
3	*ABL*	ccc ctt tct ctt cca g AA GCC CTT CAG CGG CCA

Fig.6

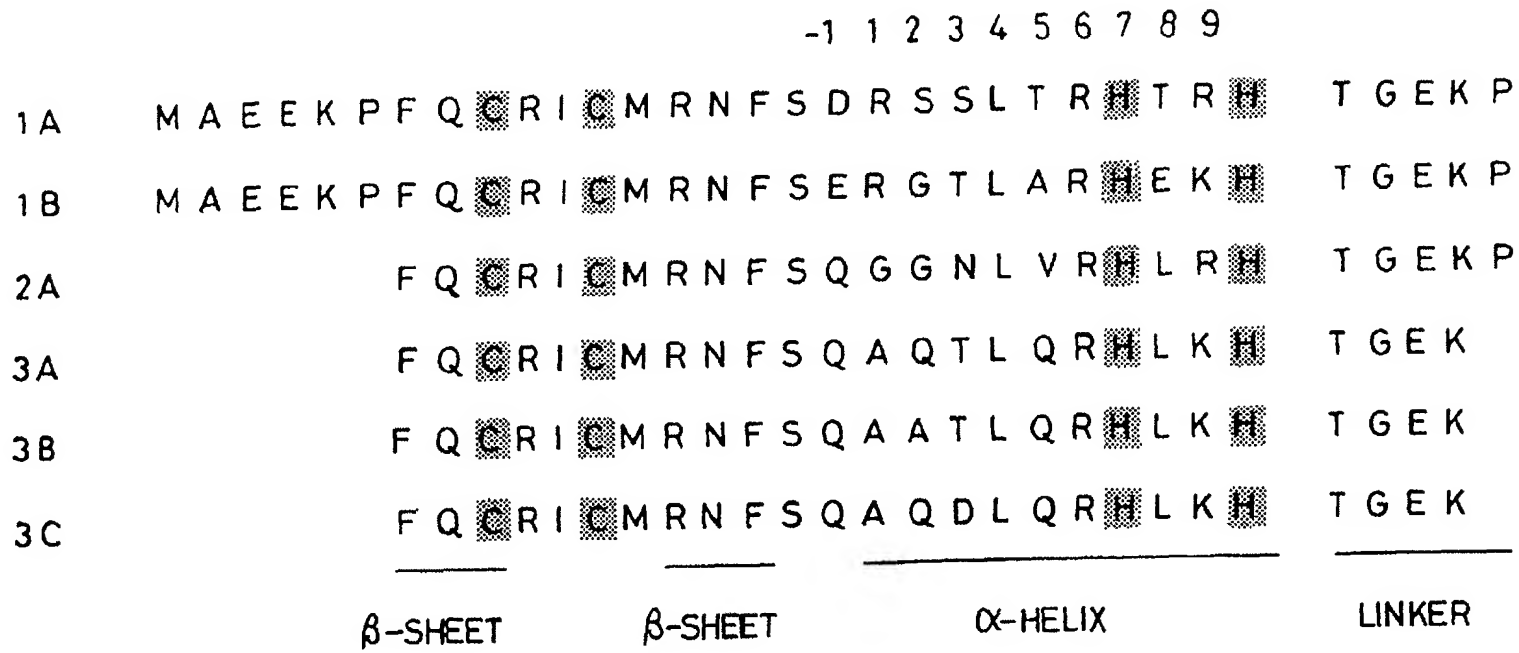


Fig. 7

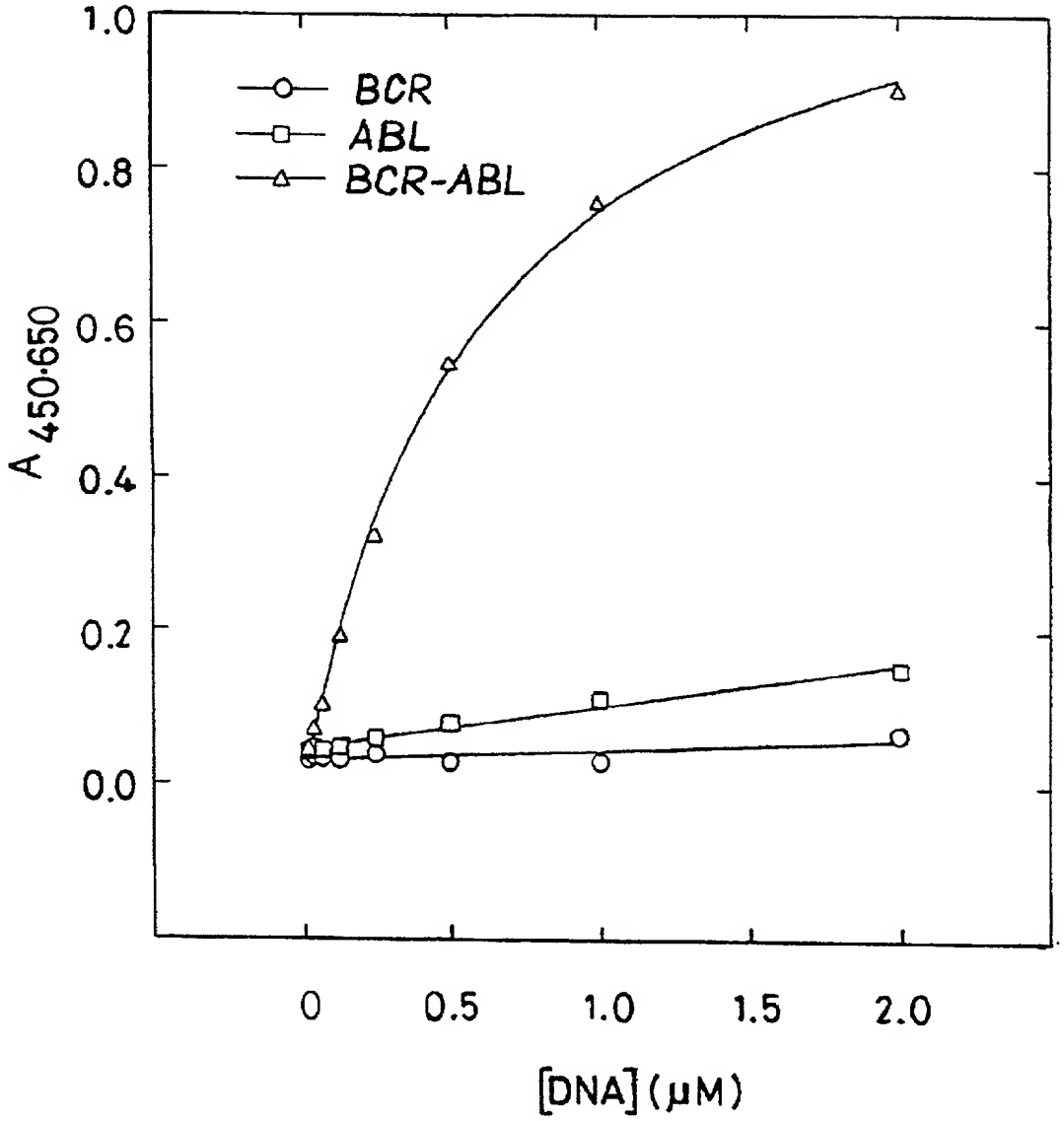
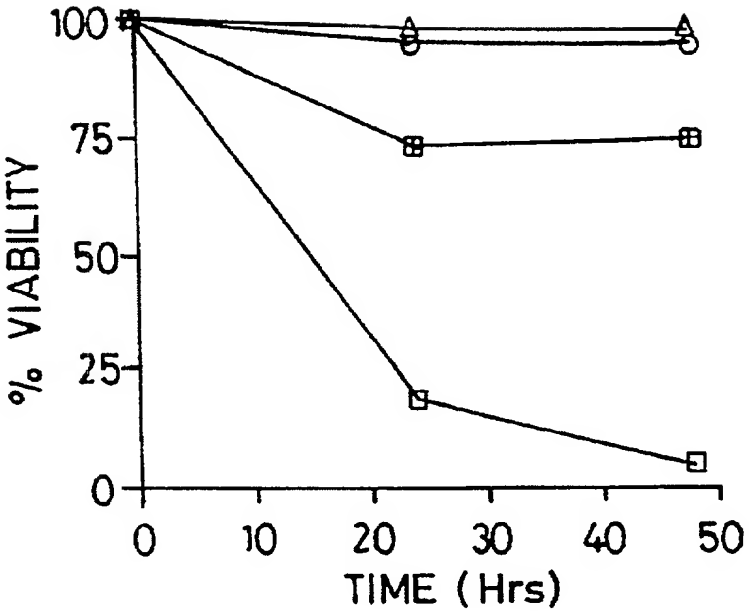


Fig. 8



Ba/F3

Ba/F3+p190

Ba/F3+p210

(Ba/F3+p210)+anti $p190^{BCR-ABL}$ peptide

(Ba/F3+p190)+anti $p190^{BCR-ABL}$ peptide

Fig. 9

Fig. 10A

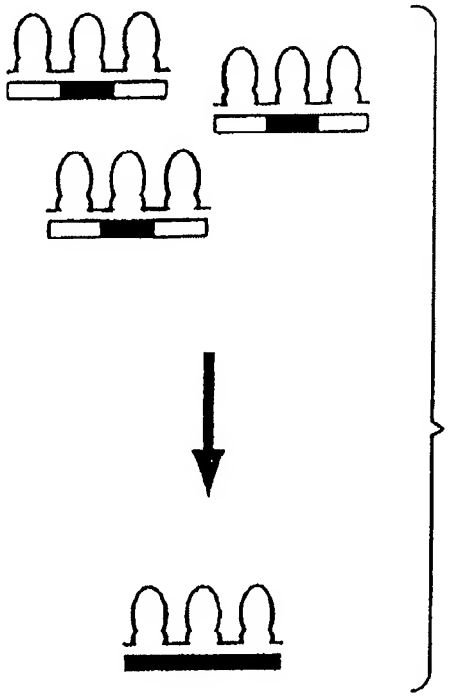


Fig. 10B

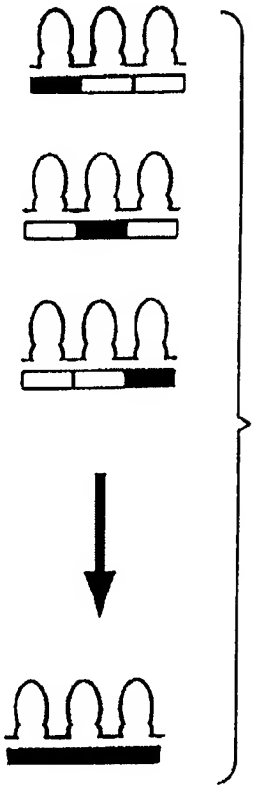


Fig. 10C

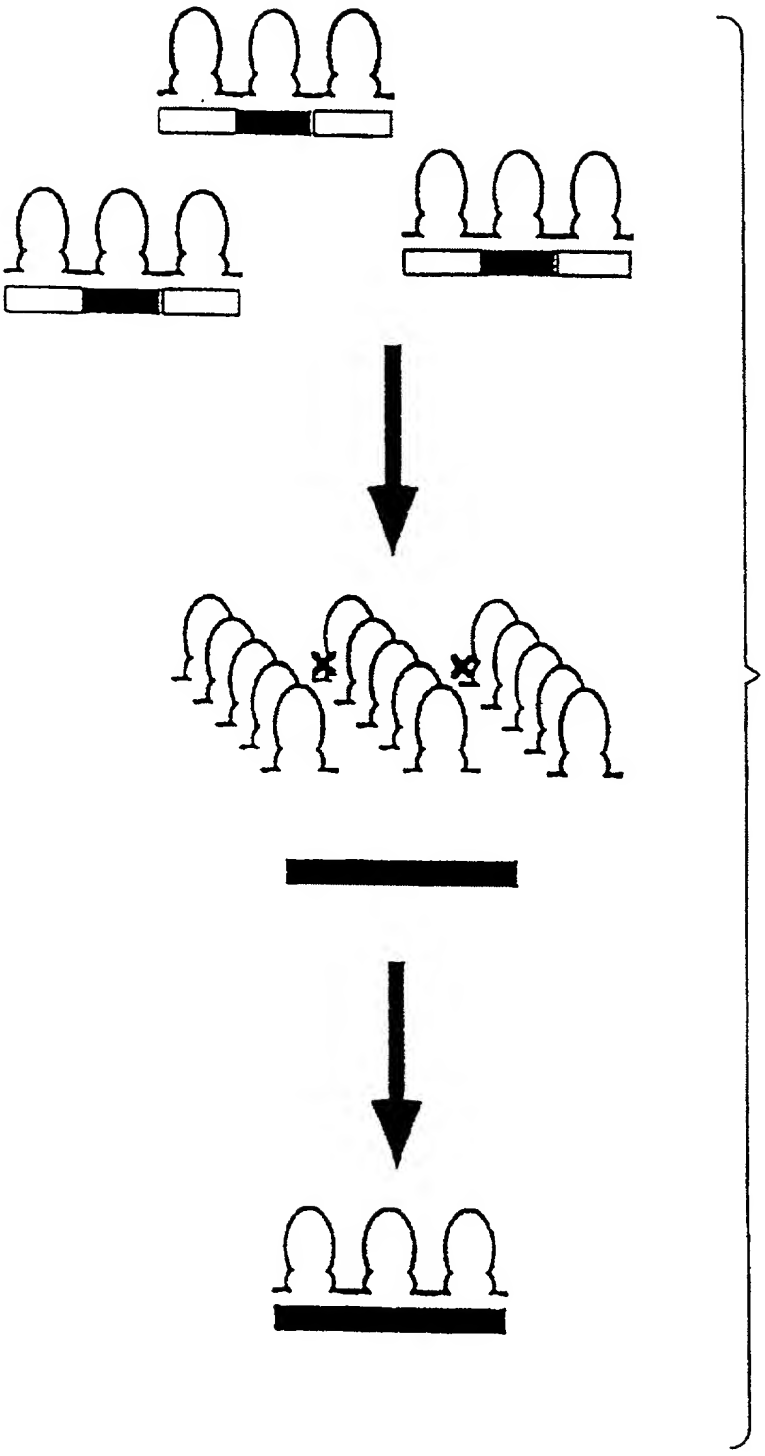


Fig.11

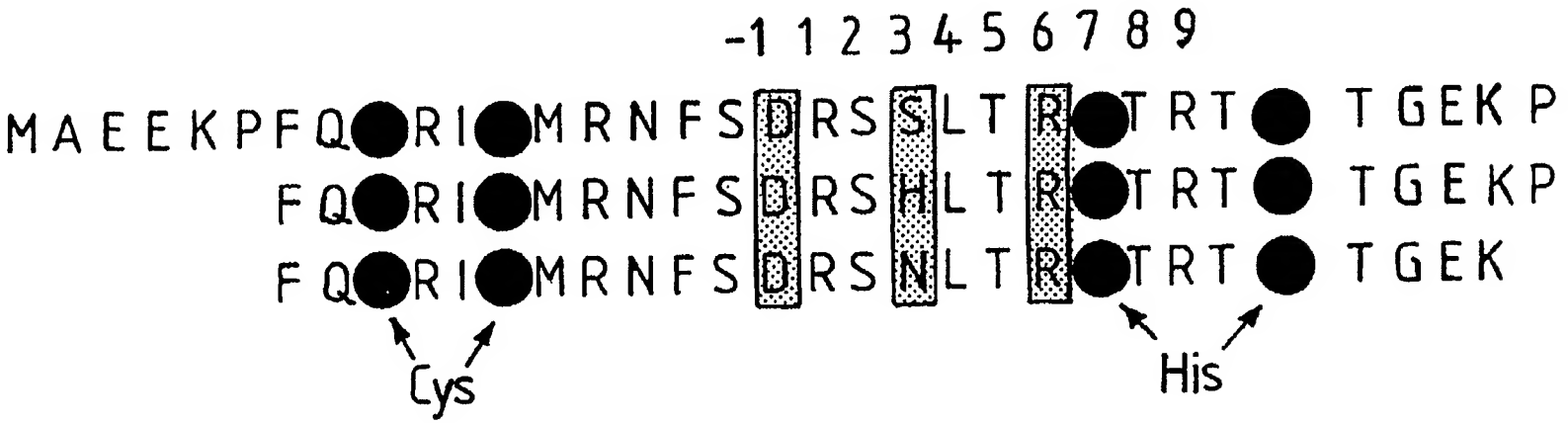

-1 1 2 3 4 5 6 7 8 9
MAEEKPFQ●RI●MRNFSDRSSLTR●TRT● TGEKP
FQ●RI●MRNFSDRSHLTR●TRT● TGEKP
FQ●RI●MRNFSDRSNLTR●TRT● TGEK
Cys
His

Fig. 12